SEQUENCE LISTING

<110> Braun, Jonathan
Sutton, Christopher L.

<120> IBD-Associated Microbial Nucleic Acid Molecules

<130> P-PM 4966

<150> US 09/303,120
<151> 1999-04-30

<150> US 09/820,576
<151> 2001-03-28

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 302
<212> DNA
<213> Unknown

<220>
<223> Microbial Organism from the human gut

<221> CDS
<222> (2)...(301)

<400> 1

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a gat ctg gcc agc gcc gtg ggc atc cag tcc ggc agc atc ttt cat cac 49
  Asp Leu Ala Ser Ala Val Gly Ile Gln Ser Gly Ser Ile Phe His His
   1               5                  10                  15

ttc aag agc aag gat gag ata ttg cgt gcc gtg atg gag gaa acc atc   97
Phe Lys Ser Lys Asp Glu Ile Leu Arg Ala Val Met Glu Glu Thr Ile
            20                  25                  30

cat tac aac acc gcg atg atg cgc gct tca ctg gag gag gcg agc acg   145
His Tyr Asn Thr Ala Met Met Arg Ala Ser Leu Glu Glu Ala Ser Thr
         35                  40                  45

gtg cgc gaa cgc gtg ctg gcg ctg atc cgc tgc gag ttg cag tcg atc   193
Val Arg Glu Arg Val Leu Ala Leu Ile Arg Cys Glu Leu Gln Ser Ile
     50                  55                  60

atg ggc ggc agt ggc gag gcc atg gcg gtg ctg gtc tac gaa tgg cgc   241
Met Gly Gly Ser Gly Glu Ala Met Ala Val Leu Val Tyr Glu Trp Arg
 65                  70                  75                  80
```

```
tcg ctg tcg gcc gaa ggc cag gcg cac gtg ctg gcc ctg cgt gac gtg   289
Ser Leu Ser Ala Glu Gly Gln Ala His Val Leu Ala Leu Arg Asp Val
                 85                  90                  95

tat gag cag atc t                                              302
Tyr Glu Gln Ile
            100
```

<210> 2
<211> 100
<212> PRT
<213> Unknown

<220>
<223> Microbial organism from the human gut

<400> 2

```
Asp Leu Ala Ser Ala Val Gly Ile Gln Ser Gly Ser Ile Phe His His
 1               5                  10                  15
Phe Lys Ser Lys Asp Glu Ile Leu Arg Ala Val Met Glu Glu Thr Ile
            20                  25                  30
His Tyr Asn Thr Ala Met Met Arg Ala Ser Leu Glu Glu Ala Ser Thr
        35                  40                  45
Val Arg Glu Arg Val Leu Ala Leu Ile Arg Cys Glu Leu Gln Ser Ile
    50                  55                  60
Met Gly Gly Ser Gly Glu Ala Met Ala Val Leu Val Tyr Glu Trp Arg
65                  70                  75                  80
Ser Leu Ser Ala Glu Gly Gln Ala His Val Leu Ala Leu Arg Asp Val
                85                  90                  95
Tyr Glu Gln Ile
            100
```

<210> 3
<211> 392
<212> DNA
<213> Unknown

<220>
<223> Microbial Organism from the human gut

<221> CDS
<222> (2)...(346)

<221> misc_feature
<222> (1)...(392)
<223> n = A,T,C or G

<400> 3

```
a gat ctt gag cgt cat gag tgc ctg ggg tac gcc ttt tca tcg cgt ccg 49
  Asp Leu Glu Arg His Glu Cys Leu Gly Tyr Ala Phe Ser Ser Arg Pro
   1               5                  10                  15
```

```
gcg gat cga gag tgg gtg ttt ttt cag ggc acg gtt tcc tac aag gta     97
Ala Asp Arg Glu Trp Val Phe Phe Gln Gly Thr Val Ser Tyr Lys Val
            20                  25                  30

cga gtg gcc agc cgt ttg ctc atc aat gaa agc cgg gca ttg atg tcg    145
Arg Val Ala Ser Arg Leu Leu Ile Asn Glu Ser Arg Ala Leu Met Ser
        35                  40                  45

gcg gca ttg gat ggt ttt ggc ata gtg ctc ggc ccg caa gac ttc ctg    193
Ala Ala Leu Asp Gly Phe Gly Ile Val Leu Gly Pro Gln Asp Phe Leu
    50                  55                  60

cga acg gcg ttg gcg agt ggc gag ttg gtg cgg gtg ttg ccg gag ttt    241
Arg Thr Ala Leu Ala Ser Gly Glu Leu Val Arg Val Leu Pro Glu Phe
65                  70                  75                  80

gag gct ccg agt cgg tcg atg cat ttg gtc tac acc gca aac cgc cag    289
Glu Ala Pro Ser Arg Ser Met His Leu Val Tyr Thr Ala Asn Arg Gln
                85                  90                  95

cgt acc gcc aag ttg cgc tgc ttt gtc gag act gtg ctg gga cgt ttt    337
Arg Thr Ala Lys Leu Arg Cys Phe Val Glu Thr Val Leu Gly Arg Phe
            100                 105                 110

ggt ccg gta tgaaggagca ccaccgtggc ggtcgccggg angcacctaa             386
Gly Pro Val
        115

agatct                                                             392
```

<210> 4
<211> 115
<212> PRT
<213> Unknown

<220>
<223> Microbial organism from the human gut

<400> 4

```
Asp Leu Glu Arg His Glu Cys Leu Gly Tyr Ala Phe Ser Ser Arg Pro
1               5                   10                  15
Ala Asp Arg Glu Trp Val Phe Phe Gln Gly Thr Val Ser Tyr Lys Val
            20                  25                  30
Arg Val Ala Ser Arg Leu Leu Ile Asn Glu Ser Arg Ala Leu Met Ser
        35                  40                  45
Ala Ala Leu Asp Gly Phe Gly Ile Val Leu Gly Pro Gln Asp Phe Leu
    50                  55                  60
Arg Thr Ala Leu Ala Ser Gly Glu Leu Val Arg Val Leu Pro Glu Phe
65                  70                  75                  80
Glu Ala Pro Ser Arg Ser Met His Leu Val Tyr Thr Ala Asn Arg Gln
                85                  90                  95
Arg Thr Ala Lys Leu Arg Cys Phe Val Glu Thr Val Leu Gly Arg Phe
```

100 105 110
Gly Pro Val
115

<210> 5
<211> 114
<212> PRT
<213> Unknown

<220>
<223> Microbial Organism from the human gut

<221> VARIANT
<222> (1)...(114)
<223> Xaa = Any Amino Acid

<400> 5
Arg Thr Arg Arg Ile Ser Leu Pro His Lys Lys Leu Ala Arg Asn Gly
1 5 10 15
Val Leu Tyr Ser His Gly Ala Thr Gln Glu Asp Ile Phe Ala Pro Cys
20 25 30
Gln His Arg Arg Cys Gln Ile Thr Lys Ala Tyr His Glu Ala Arg Leu
35 40 45
Val Glu Gln Ser Arg Arg Gln Arg Thr Ala Leu Gln His Pro His Gln
50 55 60
Arg Leu Lys Leu Ser Arg Thr Pro Arg His Met Gln Asp Val Gly Cys
65 70 75 80
Val Ala Leu Thr Gly Gly Leu Gln Ala Ala Lys Asp Leu Ser His Gln
85 90 95
Ser Thr Lys Thr Arg Tyr Ser Pro Ala Gly Gly His Arg Asp Gly Pro
100 105 110
Xaa Val

<210> 6
<211> 190
<212> PRT
<213> Clostridium pasteurianum

<400> 6
Met Asn Lys Thr Lys Asp Asn Ile Phe Tyr Ser Ala Ile Lys Val Phe
1 5 10 15
Ser Asn Asn Gly Tyr Asn Gly Ala Thr Met Asp Glu Ile Ala Ser Asn
20 25 30
Ala Gly Val Ala Lys Gly Thr Leu Tyr Tyr His Phe Lys Ser Lys Glu
35 40 45
Glu Ile Phe Lys Tyr Ile Ile Glu Glu Gly Val Asn Leu Met Lys Asn
50 55 60
Glu Ile Asp Glu Ala Thr Asp Lys Glu Lys Thr Ala Leu Glu Lys Leu
65 70 75 80
Lys Ala Val Cys Arg Val Gln Leu Asn Leu Ile Tyr Lys Asn Arg Asp

```
                85                  90                  95
Phe Phe Lys Val Ile Ala Ser Gln Leu Trp Gly Lys Glu Leu Arg Gln
            100                 105                 110
Leu Glu Leu Arg Asp Ile Met Arg Asn Tyr Val Val His Ile Glu Glu
        115                 120                 125
Phe Val Lys Asp Ala Met Glu Ala Gly Ser Ile Lys Lys Gly Asn Ser
    130                 135                 140
Leu Phe Val Ala Tyr Ala Phe Leu Gly Thr Leu Cys Ser Val Ser Leu
145                 150                 155                 160
Tyr Glu Val Ile Asn Ala Glu Asn Asp Asn Ile Asn Asn Thr Ile Glu
                165                 170                 175
Asn Leu Met Asn Tyr Ile Leu Asn Gly Ile Gly Leu Gln Asn
            180                 185                 190
```

<210> 7
<211> 200
<212> PRT
<213> Mycobacterium tuberculosis

<400> 7

```
Met Asp Arg Val Ala Gly Gln Val Asn Ser Arg Arg Gly Glu Leu Leu
 1               5                  10                  15
Glu Leu Ala Ala Ala Met Phe Ala Glu Arg Gly Leu Arg Ala Thr Thr
            20                  25                  30
Val Arg Asp Ile Ala Asp Gly Ala Gly Ile Leu Ser Gly Ser Leu Tyr
        35                  40                  45
His His Phe Ala Ser Lys Glu Glu Met Val Asp Glu Leu Leu Arg Gly
    50                  55                  60
Phe Leu Asp Trp Leu Phe Ala Arg Tyr Arg Asp Ile Val Asp Ser Thr
65                  70                  75                  80
Ala Asn Pro Leu Glu Arg Leu Gln Gly Leu Phe Met Ala Ser Phe Glu
                85                  90                  95
Ala Ile Glu His His His Ala Gln Val Val Ile Tyr Gln Asp Glu Ala
            100                 105                 110
Gln Arg Leu Ala Ser Gln Pro Arg Phe Ser Tyr Ile Glu Asp Arg Asn
        115                 120                 125
Lys Gln Gln Arg Lys Met Trp Val Asp Val Leu Asn Gln Gly Ile Glu
    130                 135                 140
Glu Gly Tyr Phe Arg Pro Asp Leu Asp Val Asp Leu Val Tyr Arg Phe
145                 150                 155                 160
Ile Arg Asp Thr Thr Trp Val Ser Val Arg Trp Tyr Arg Pro Gly Gly
                165                 170                 175
Pro Leu Thr Ala Gln Gln Val Gly Gln Gln Tyr Leu Ala Ile Val Leu
            180                 185                 190
Gly Gly Ile Thr Lys Glu Gly Val
        195                 200
```

<210> 8
<211> 192
<212> PRT
<213> Auifex aeolicus

<400> 8

```
Met Tyr Ile Leu Leu Phe Met Gly Glu Lys Arg Ser Asp Thr Lys Glu
 1               5                  10                  15
Lys Ile Leu Ser Ser Ala Leu Lys Leu Phe Ser Lys Lys Gly Phe Lys
            20                  25                  30
Glu Thr Thr Ile Lys Asp Ile Ala Lys Glu Val Gly Ile Thr Glu Gly
        35                  40                  45
Ala Ile Tyr Arg His Phe Thr Ser Lys Glu Glu Ile Ile Lys Ser Leu
    50                  55                  60
Leu Glu Ser Ile Thr Lys Glu Leu Arg His Lys Leu Glu Val Ala Leu
65                  70                  75                  80
Gln Arg Gly Glu Thr Asp Glu Glu Ile Leu Glu Ser Ile Val Asp Thr
                85                  90                  95
Leu Ile Asp Tyr Ala Phe Ser Asn Pro Glu Ser Phe Arg Phe Leu Asn
            100                 105                 110
Leu Tyr His Leu Leu Lys Glu Tyr Gly Glu Val Lys Asn Leu Pro Gly
        115                 120                 125
Glu Leu Ile Leu Lys Phe Leu Asn Gly Leu Tyr Leu Lys Arg Lys Leu
    130                 135                 140
Lys Thr Tyr Pro Glu Ile Ala Leu Ala Val Val Thr Gly Ser Val Glu
145                 150                 155                 160
Arg Val Phe Ile Phe Lys Glu Arg Asn Phe Leu Asp Tyr Asp Glu Glu
                165                 170                 175
Thr Ile Lys Lys Glu Leu Lys Lys Val Leu Lys Ser Ala Ile Leu Ala
            180                 185                 190
```

<210> 9
<211> 18
<212> DNA
<213> Unknown

<220>
<223> Microbial Organism from the human gut

<400> 9
ccgtgggcat ccagtccg 18

<210> 10
<211> 19
<212> DNA
<213> Unknown

<220>
<223> Microbial Organism from the human gut

<400> 10
tctgctcata cacgtcacg 19